*Corrections*

2013. **Growth of Large and Highly Ordered 2D Crystals of a K+ Channel, Structural Role of Lipidic Environment**. De Zorzi R, Nicholson WV, Guigner JM, Erne-Brand F, Stahlberg H, Benien-Bryan C. *Biophys J.* 105(2): 398–408

Author list should read:

Rita De Zorzi, William V. Nicholson, Jean-Michel Guigner, Françoise Erne-Brand, Catherine Vénien-Bryan

Removal of author: Henning Stahlberg, Center for Cellular Imaging and Nano Analytics (C-CINA), Biozentrum, University of Basel, Basel, Switzerland. Stahlberg was not involved in data collection, data analysis, or data interpretation of our work, nor in the manuscript writing. Upon Stahlberg's request, he is being removed from the author list.

http://dx.doi.org/10.1016/j.bpj.2013.08.005

2011. **Effects of macromolecular crowding on an intrinsically disordered protein characterized by small-angle neutron scattering with contrast matching**. Johansen D, Jeffries CMJ, Hammouda B, Trewhella J, and Goldenberg DP. *Biophys. J.* 100(4):1120–1128.

Fig. 4 of the original paper showed the results of a computational simulation of crowding effects on a disordered protein, the N protein of bacteriophage λ, and Fig. 5 showed the results of fitting experimental small-angle neutron scattering (SANS) data to those predicted by the simulations. Upon reexamining the computational data, the authors have discovered an error in a computer program used in the simulations. This error led to a significant overestimate of the radius of the equivalent sphere used to represent the excluded volumes of the disordered protein molecules and, in turn, an overestimate of the predicted changes in the distribution of conformations making up the disordered ensemble. The corrected figures are shown here.

The predictions illustrated in Fig. 4 of the original paper indicated that crowding by a solution of spheres with 15 Å radius would lead to a reduction in the RMS radius of gyration of the protein by as much as 35% at the highest simulated crowding density, with the volume fraction occupied by the spheres (φ) equal to 0.2. In contrast, the corrected calculations lead to a predicted reduction of only 11% in the mean radius of gyration. Similarly, the corrected simulation predicts an increase in the fractal dimension ($D_m$) from 1.66 for the uncrowded disordered protein to 1.91 for the most highly crowded condition (φ=0.2), as compared to the original prediction of $D_m$=2.7. The correction in the simulation also leads to significantly better agreement with the experimental data presented in the original manuscript (Fig. 5). In particular, the small changes in the

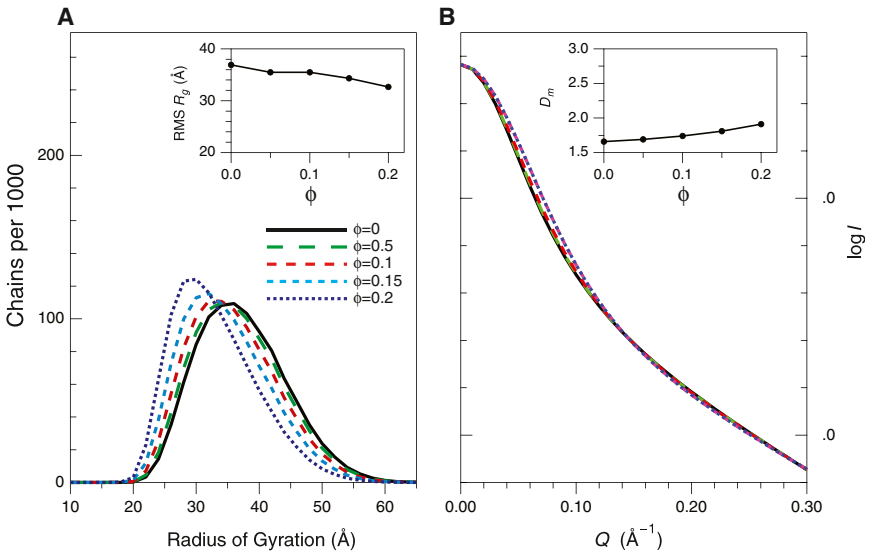


FIGURE 4 Computational simulation of molecular crowding effects. (*A*) Distribution of calculated conformations, as defined by the radius of gyration. The solid black curve represents the unweighted distribution of approximately 230,000 conformations, expressed as the number of chains per 1000 with radii of gyration lying within an interval of 1 Å. The weighted distributions represented by the dashed curves for different crowding densities were calculated from the excluded covolumes of the individual conformations and a spherical crowding molecule with a radius of 15 Å, as described in the text. The inset shows the RMS radius gyration of the weighted ensembles as a function of crowding density. (*B*) Simulated SANS profiles calculated from the individual conformations and Boltzmann weighting factors for the indicated crowding densities. The inset shows the fractal dimension, $D_m$, calculated from the simulated scattering curves, as a function of φ.